

Heidi Dvinge

List of Publications by Year in descending order

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17
papers

6,083
citations

567281

15
h-index

888059

17
g-index

17
all docs

17
docs citations

17
times ranked

13403
citing authors

#	ARTICLE	IF	CITATIONS
1	Alternative Splicing and Cleavage of GLUT8. <i>Molecular and Cellular Biology</i> , 2021, 41, .	2.3	14
2	Human spliceosomal snRNA sequence variants generate variant spliceosomes. <i>Rna</i> , 2021, 27, 1186-1203.	3.5	12
3	RNA components of the spliceosome regulate tissue- and cancer-specific alternative splicing. <i>Genome Research</i> , 2019, 29, 1591-1604.	5.5	96
4	Coordinated alterations in RNA splicing and epigenetic regulation drive leukaemogenesis. <i>Nature</i> , 2019, 574, 273-277.	27.8	149
5	Regulation of alternative <sc>mRNA</sc> splicing: old players and new perspectives. <i>FEBS Letters</i> , 2018, 592, 2987-3006.	2.8	71
6	Modulation of splicing catalysis for therapeutic targeting of leukemia with mutations in genes encoding spliceosomal proteins. <i>Nature Medicine</i> , 2016, 22, 672-678.	30.7	301
7	RNA splicing factors as oncoproteins and tumour suppressors. <i>Nature Reviews Cancer</i> , 2016, 16, 413-430.	28.4	549
8	Integrative Clinical Genomics of Advanced Prostate Cancer. <i>Cell</i> , 2015, 161, 1215-1228.	28.9	2,660
9	Widespread intron retention diversifies most cancer transcriptomes. <i>Genome Medicine</i> , 2015, 7, 45.	8.2	283
10	The shaping and functional consequences of the microRNA landscape in breast cancer. <i>Nature</i> , 2013, 497, 378-382.	27.8	370
11	NuRD-mediated deacetylation of H3K27 facilitates recruitment of Polycomb Repressive Complex 2 to direct gene repression. <i>EMBO Journal</i> , 2012, 31, 593-605.	7.8	224
12	Genome-wide characterization of Foxa2 targets reveals upregulation of floor plate genes and repression of ventrolateral genes in midbrain dopaminergic progenitors. <i>Development (Cambridge)</i> , 2012, 139, 2625-2634.	2.5	55
13	PeakAnalyzer: Genome-wide annotation of chromatin binding and modification loci. <i>BMC Bioinformatics</i> , 2010, 11, 415.	2.6	210
14	Systematic comparison of microarray profiling, real-time PCR, and next-generation sequencing technologies for measuring differential microRNA expression. <i>Rna</i> , 2010, 16, 991-1006.	3.5	588
15	Mapping Organelle Proteins and Protein Complexes in <i>Drosophila melanogaster</i>. <i>Journal of Proteome Research</i> , 2009, 8, 2667-2678.	3.7	71
16	<i>HTqPCR</i>: high-throughput analysis and visualization of quantitative real-time PCR data in R. <i>Bioinformatics</i> , 2009, 25, 3325-3326.	4.1	205
17	Modeling of C/EBP β Mutant Acute Myeloid Leukemia Reveals a Common Expression Signature of Committed Myeloid Leukemia-Initiating Cells. <i>Cancer Cell</i> , 2008, 13, 299-310.	16.8	225